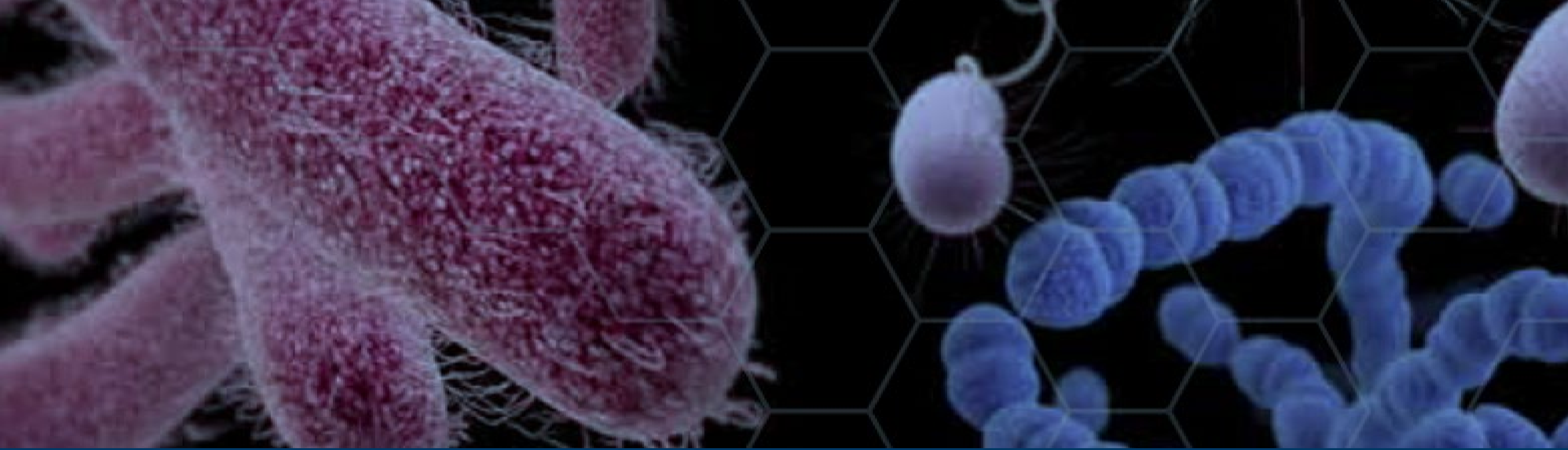


Applications of Pathogen Genomics in Public Health: State Level

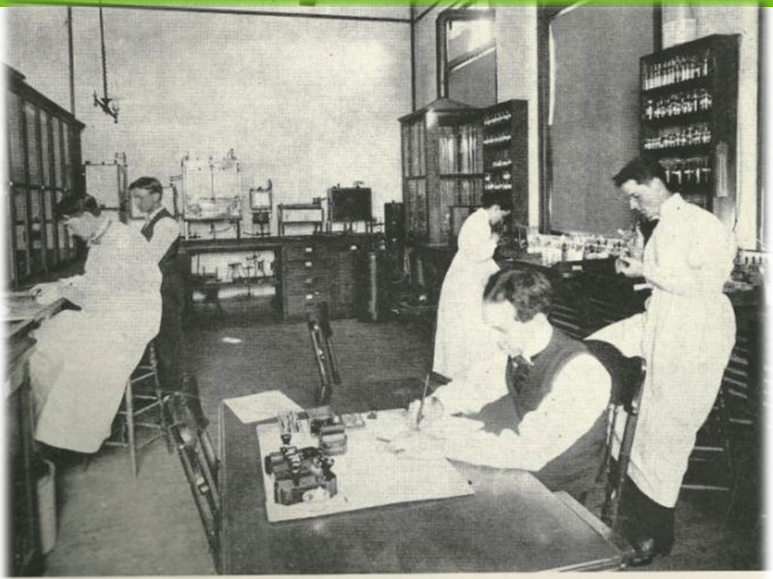
Ruth Lynfield, MD

State Epidemiologist and Medical Director

DEPARTMENT
OF HEALTH

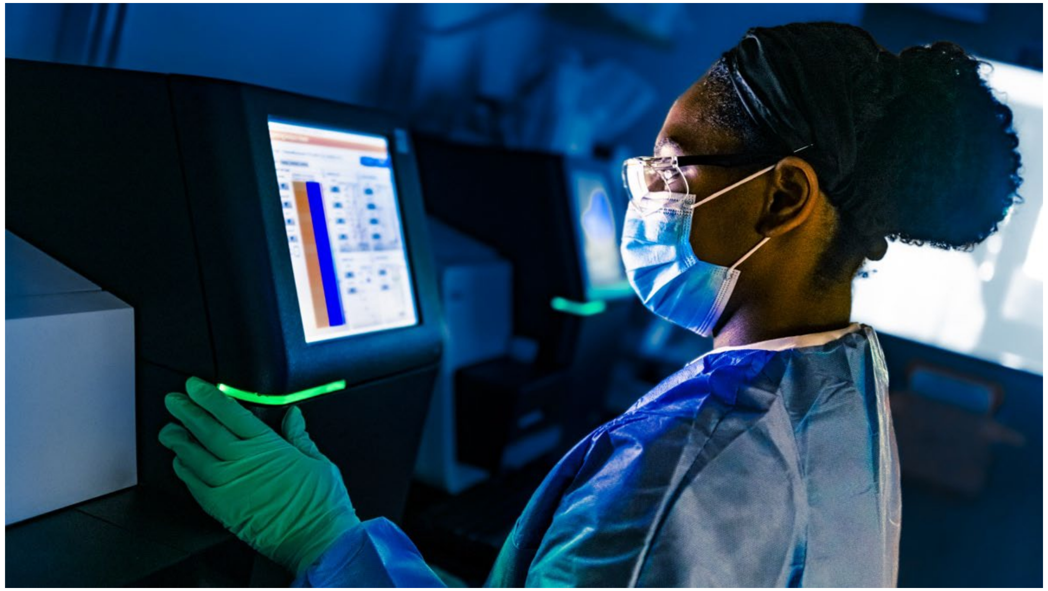
health.state.mn.us

State Public Health



MINNESOTA DEPARTMENT OF HEALTH LABORATORY IN THE 1890s
A. W. Miller, Harry Charleston, Orianna McDaniel, W. P. Moorhead, L. B. Wilson
Courtesy Minnesota Department of Health

- Diagnostic testing of specimens, characterization of isolates
- Surveillance of infectious diseases
- Investigation of clusters, outbreaks
- Applied research to improve population health

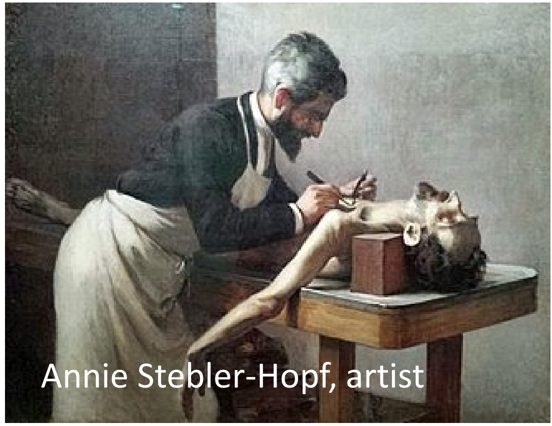


State Public Health (cont.)

Epidemiologists use surveillance and other data to study patterns of disease incidence to develop and evaluate **prevention and control strategies**

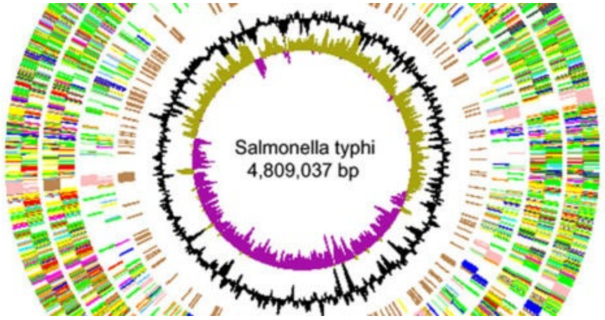
Evolution of Epidemiological Approaches

- 19th Century: Clinical and epidemiological definitions of syndromes

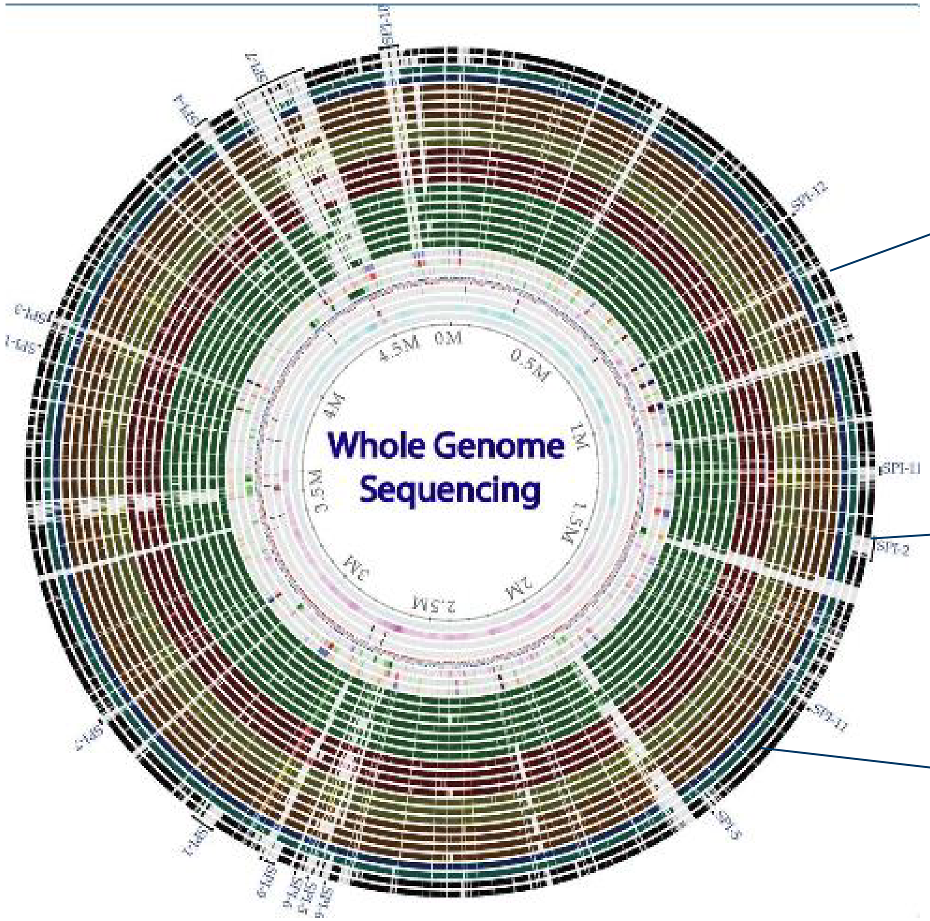

Annie Stebler-Hopf, artist

- 20th Century: Incorporating microbiological characterization

- 21st Century: Incorporating pathogen genomics



Some Advantages of Whole Genome Sequencing (WGS)



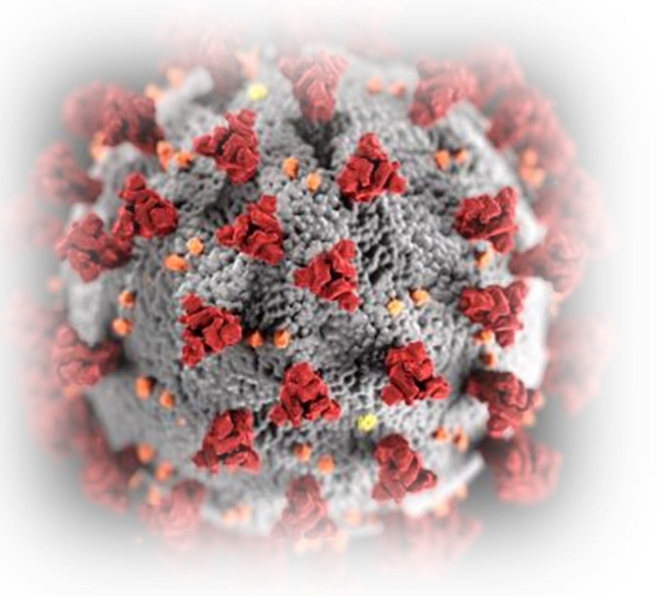
Relatedness of strains: outbreak investigation, evolutionary history

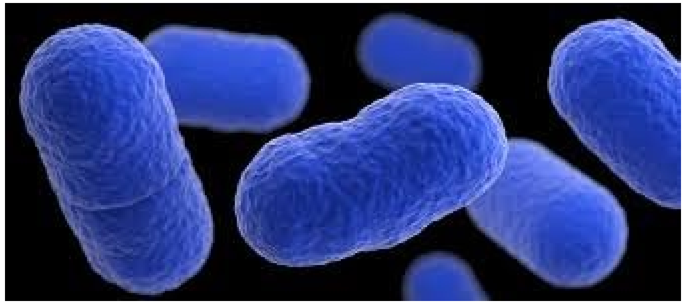
Identification of virulence factors

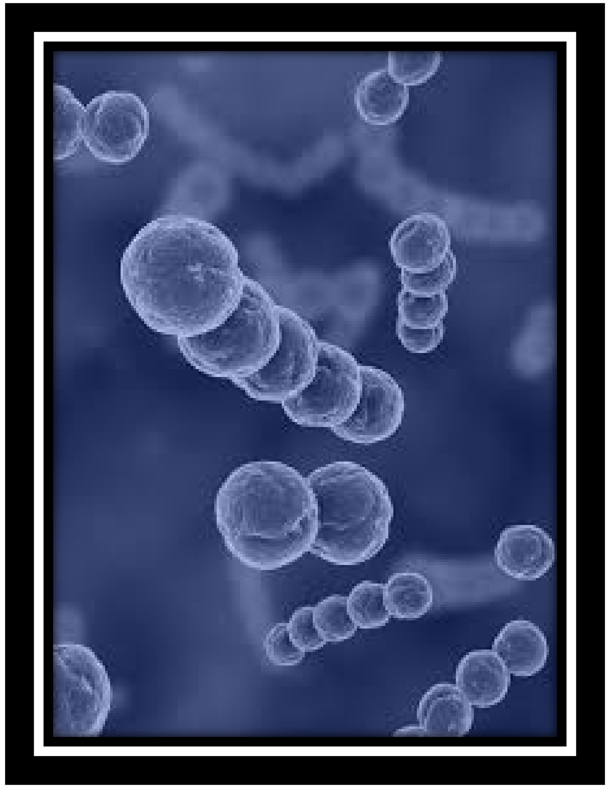
Antibiotic resistance genes

Collaboration of Epidemiology, Laboratory, and Bioinformatics

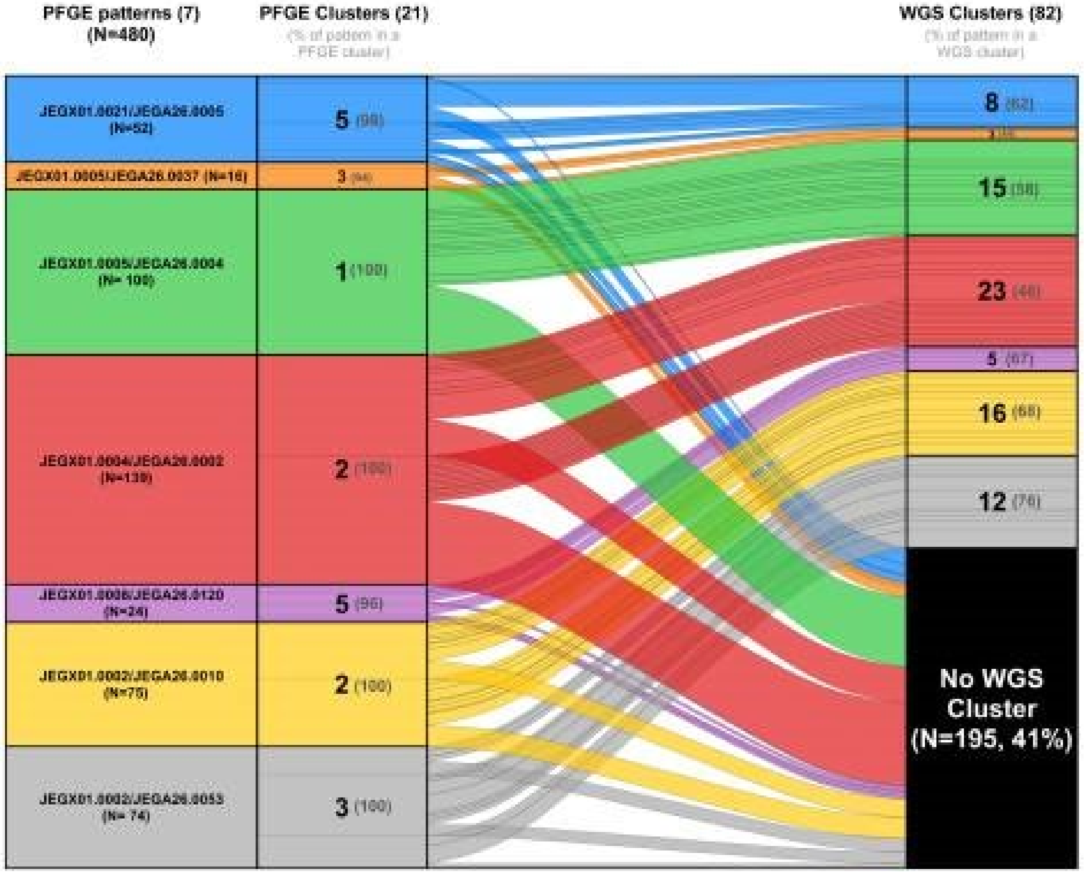
Some Examples



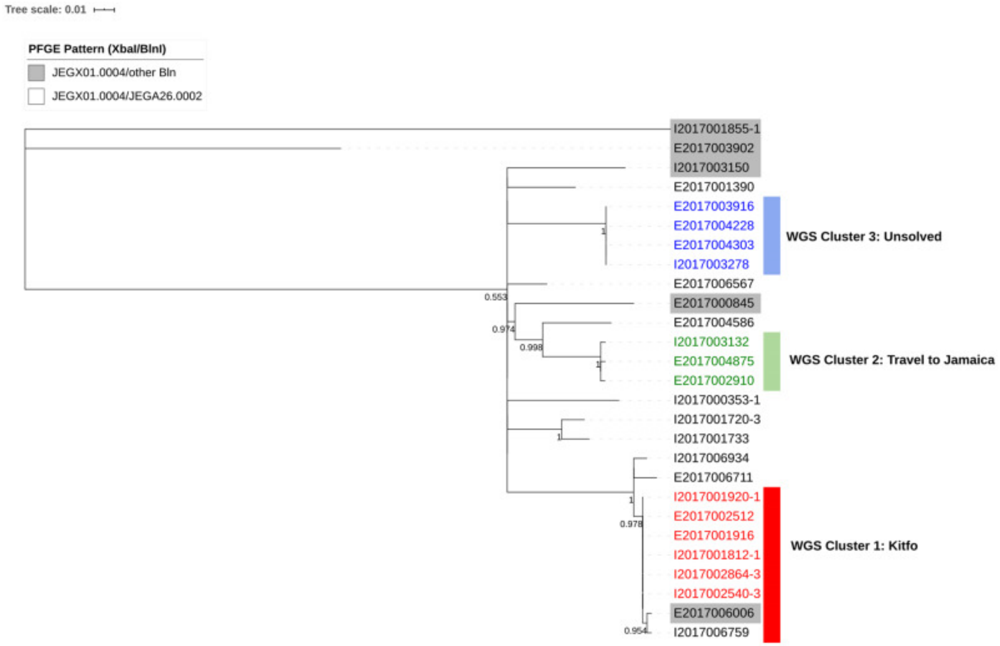




PFGE vs. WGS, S. Enteritidis



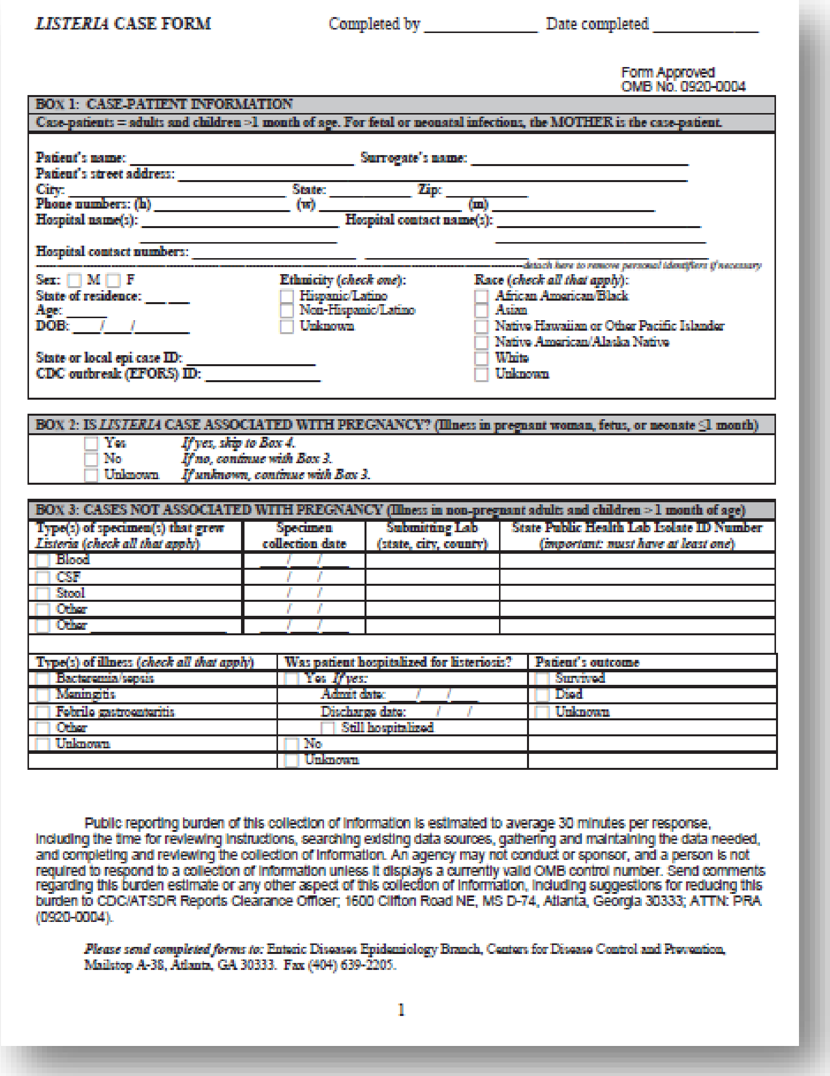
- WGS achieves higher resolution compared to traditional PFGE
- More accurate cluster identification



Rounds, et al. Epidemiol Infect. 2020; 148: e254.

Listeriosis Case - Routine Disease Surveillance
March 2024

- Pregnant with positive blood culture for *L. monocytogenes*
- Fetal demise at 29 weeks gestation
- Interviewed in Spanish with standardized “Listeria Initiative” national questionnaire
  - Exposure history: queso fresco (Walmart)
  - Demographics: Hispanic (Ecuador)
  - Part of current national queso fresco/cotija cheese outbreak?



LISTERIA CASE FORM Completed by ____________ Date completed ____________

Form Approved
OMB No. 0920-0004

BOX 1: CASE-PATIENT INFORMATION

Case-patients = adults and children >1 month of age. For fetal or neonatal infections, the MOTHER is the case-patient.

Patient's name: ______________________ **Surrogate's name:** ______________________
Patient's street address: ______________________
City: ______________ **State:** ________ **Zip:** ________
Phone numbers: (h) ____________ **(w)** ____________ **(m)** ____________
Hospital name(s): ______________________ **Hospital contact name(s):** ______________________
Hospital contact numbers: ____________ ____________ ____________

---detach here to remove personal identifiers if necessary

Sex: ☐ M ☐ F
State of residence: __ __
Age: _____
DOB: ___/___/______

Ethnicity (*check one*):
☐ Hispanic/Latino
☐ Non-Hispanic/Latino
☐ Unknown

Race (*check all that apply*):
☐ African American/Black
☐ Asian
☐ Native Hawaiian or Other Pacific Islander
☐ Native American/Alaska Native
☐ White
☐ Unknown

State or local epi case ID: ______________
CDC outbreak (EFORS) ID: ______________

BOX 2: IS *LISTERIA* CASE ASSOCIATED WITH PREGNANCY? (Illness in pregnant woman, fetus, or neonate ≤1 month)

☐ Yes *If yes, skip to Box 4.*
☐ No *If no, continue with Box 3.*
☐ Unknown *If unknown, continue with Box 3.*

BOX 3: CASES NOT ASSOCIATED WITH PREGNANCY (Illness in non-pregnant adults and children >1 month of age)

Type(s) of specimen(s) that grew *Listeria (check all that apply)*	Specimen collection date	Submitting Lab (state, city, county)	State Public Health Lab Isolate ID Number *(important: must have at least one)*
☐ Blood	___/___/___		
☐ CSF	/ /		
☐ Stool	/ /		
☐ Other	/ /		
☐ Other ____________	___/___/___		

Type(s) of illness *(check all that apply)*	Was patient hospitalized for listeriosis?	Patient's outcome
☐ Bacteremia/sepsis	☐ Yes *If yes:*	☐ Survived
☐ Meningitis	Admit date: ___/___/___	☐ Died
☐ Febrile gastroenteritis	Discharge date: / /	☐ Unknown
☐ Other	☐ Still hospitalized	
☐ Unknown	☐ No	
	☐ Unknown	

Public reporting burden of this collection of information is estimated to average 30 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to a collection of information unless it displays a currently valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to CDC/ATSDR Reports Clearance Officer; 1600 Clifton Road NE, MS D-74, Atlanta, Georgia 30333; ATTN: PRA (0920-0004).

Please send completed forms to: Enteric Diseases Epidemiology Branch, Centers for Disease Control and Prevention, Mailstop A-38, Atlanta, GA 30333. Fax (404) 639-2205.

1

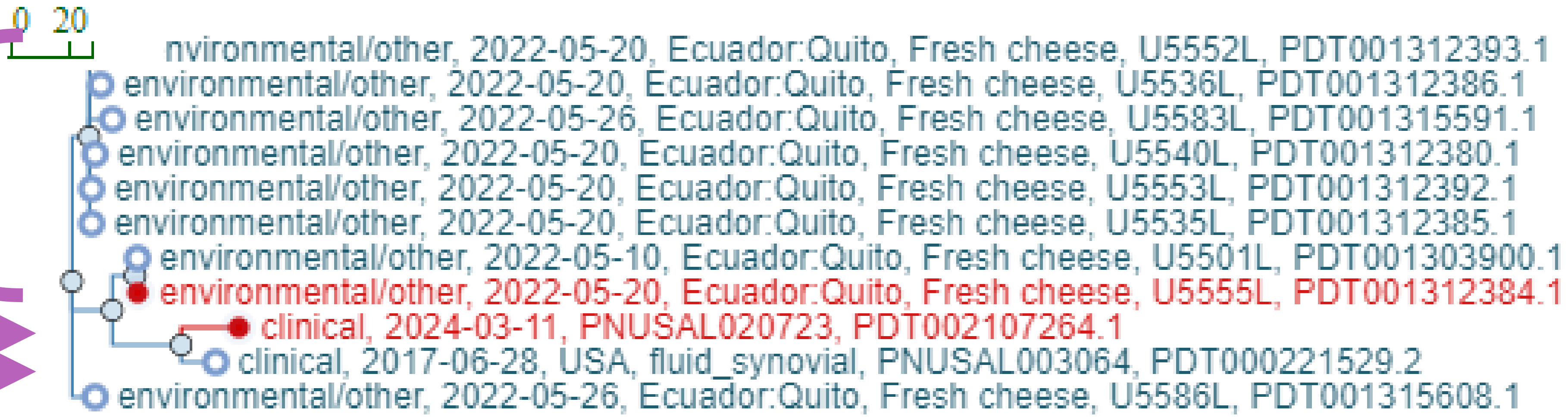
Enter Whole Genome Sequencing (WGS)….

- NCBI shows additional closely-related isolates (0-38 SNPs)
  - Not part of national queso fresco outbreak

Fresh cheese (2022) Quito, Ecuador

MN case (2024)

OR case (2017)



nvironmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5552L, PDT001312393.1
environmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5536L, PDT001312386.1
environmental/other, 2022-05-26, Ecuador:Quito, Fresh cheese, U5583L, PDT001315591.1
environmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5540L, PDT001312380.1
environmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5553L, PDT001312392.1
environmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5535L, PDT001312385.1
environmental/other, 2022-05-10, Ecuador:Quito, Fresh cheese, U5501L, PDT001303900.1
environmental/other, 2022-05-20, Ecuador:Quito, Fresh cheese, U5555L, PDT001312384.1
clinical, 2024-03-11, PNUSAL020723, PDT002107264.1
clinical, 2017-06-28, USA, fluid_synovial, PNUSAL003064, PDT000221529.2
environmental/other, 2022-05-26, Ecuador:Quito, Fresh cheese, U5586L, PDT001315608.1

- Oregon case:
  - Consumed queso fresco in Ecuador prior to infection

Re-interview Minnesota Case

<u>During entire pregnancy:</u>
Any travel to Ecuador?
Any food from Ecuador?

Yes, purchased Ecuadorian queso chonero on Facebook (5-6 months ago).

Queso chonero =
fresh cheese/queso fresco

Brick and Mortar Store in Chicago
FDA sampled cheese from Chicago location

- Positive *L. monocytogenes*
  - 1-2 SNPs from Minnesota case isolate

Public Health Interventions

- FDA import alert, ongoing investigation

U.S. FOOD & DRUG ADMINISTRATION

Import Alert 12-10

Desc: Queso Chonero Special White Cheese (Fresh Hard White Cheese)
Problems: LISTERIA : MONOCYTOGENES;
12 C - - 13 Cheese, Hispanic/Latino/Mexican Style, all varieties, including queso
Date Published: 06/06/2024

- Incidence of listeriosis in Ecuador unknown (no national surveillance)

- MDH social media and Spanish language media communications

NO COMA

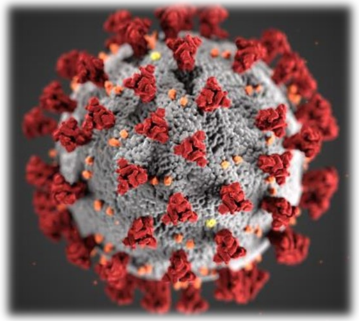
Do Not Eat

No coma Queso Chonero blanco especial importado de Ecuador.

Do not eat Queso Chonero Special White Cheese imported from Ecuador.

A *Listeria* infection in an adult from Minnesota has been linked to this cheese.

Una infección por *Listeria* en un adulto de Minnesota se ha relacionado con este queso.



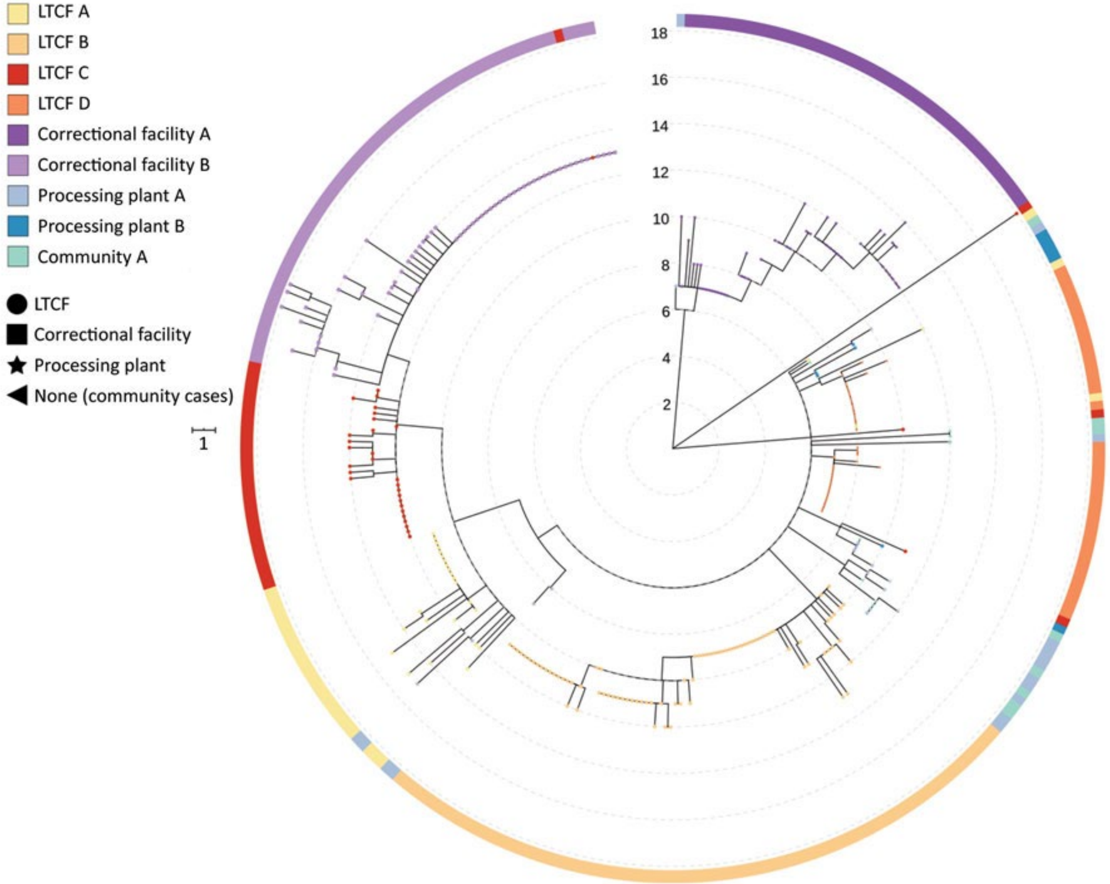
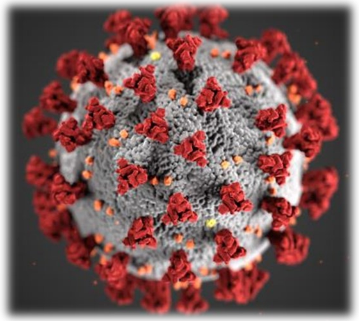


Figure 1. Phylogenetic tree of severe acute respiratory syndrome coronavirus 2 associated with selected outbreaks in Minnesota, USA, March 6–June 30, 2020. IQ-TREE (29) was used with the general time reversible substitution model for tree generation. Branch lengths were scaled to represent number of single-nucleotide mutations as shown in the scale key. LTCF, long-term care facility.

Lehnertz NB, Wang X, Garfin J, Taylor J, Zipprich J, VonBank B, et al. Transmission Dynamics of Severe Acute Respiratory Syndrome Coronavirus 2 in High-Density Settings, Minnesota, USA, March–June 2020. Emerg Infect Dis. 2021;27(8):2052-2063. https://doi.org/10.3201/eid2708.204838



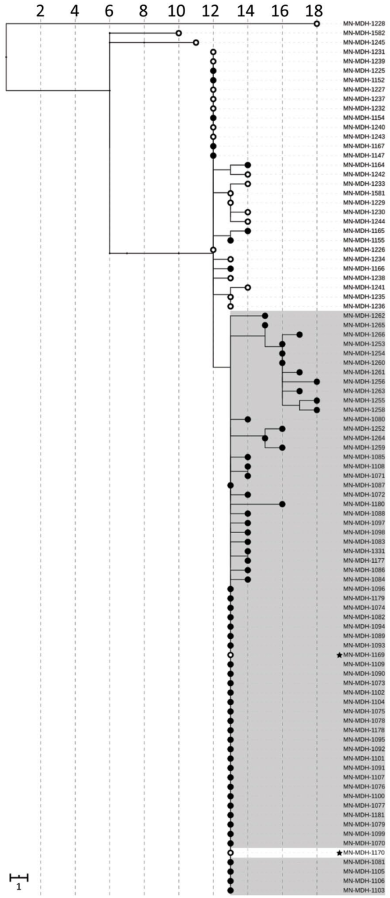
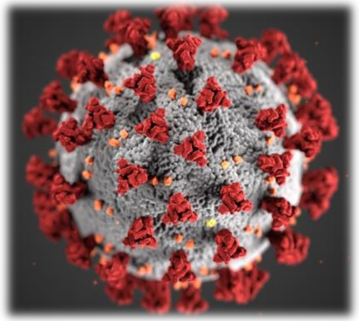


Figure 5. Phylogenetic tree of severe acute respiratory syndrome coronavirus 2 genome sequences associated with long-term care facility C and correctional facility B, Minnesota, US, April–June 2020. Filled circles represent sequences from samples from inmates or residents; open circles represent sequences from facility staff or healthcare workers. Sequences from long-term care facility C are shown on a white background; sequences from correctional facility B, on a gray background. Sequences from 2 household contacts are noted with stars. IQ-TREE (29) was used with the general time reversible substitution model for tree generation. Branch lengths were scaled to represent number of single-nucleotide mutations, as shown in the scale. MDH, Minnesota Department of Health.

Lehnertz NB, Wang X, Garfin J, Taylor J, Zipprich J, VonBank B, et al. Transmission Dynamics of Severe Acute Respiratory Syndrome Coronavirus 2 in High-Density Settings, Minnesota, USA, March–June 2020. Emerg Infect Dis. 2021;27(8):2052-2063. https://doi.org/10.3201/eid2708.204838



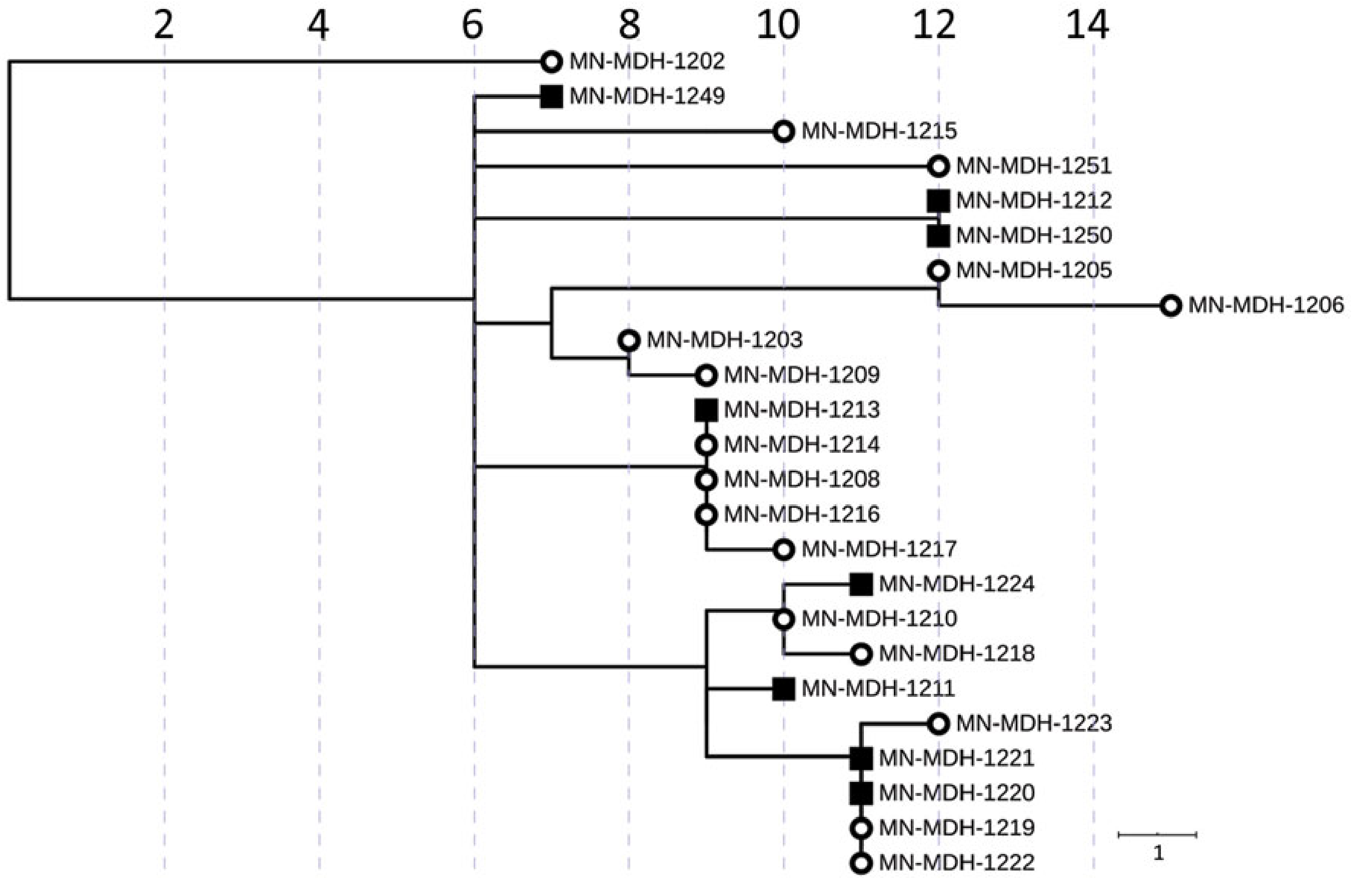
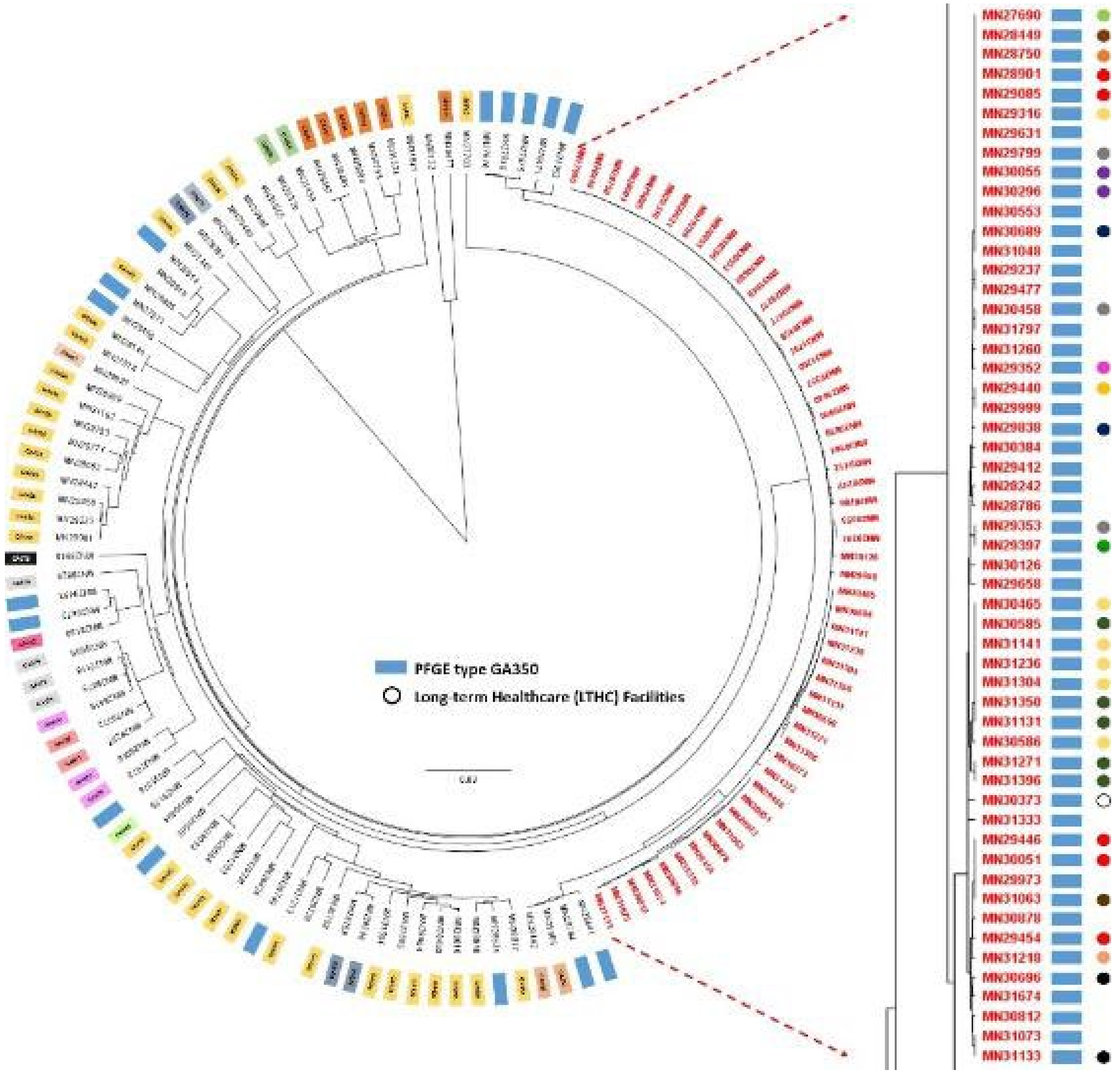


Figure 6. Phylogenetic tree of SARS-CoV-2 genome sequences associated with meat-processing plant A and the surrounding community, Minnesota, USA, March 15–June 30, 2020. Open circles represent sequences from samples from staff at processing plant A; squares represent sequences from samples from persons in the surrounding community. IQ-TREE (29) was used with the general time reversible substitution model for tree generation. Branch lengths were scaled to represent number of single-nucleotide mutations, as shown in the scale. MDH, Minnesota Department of Health.

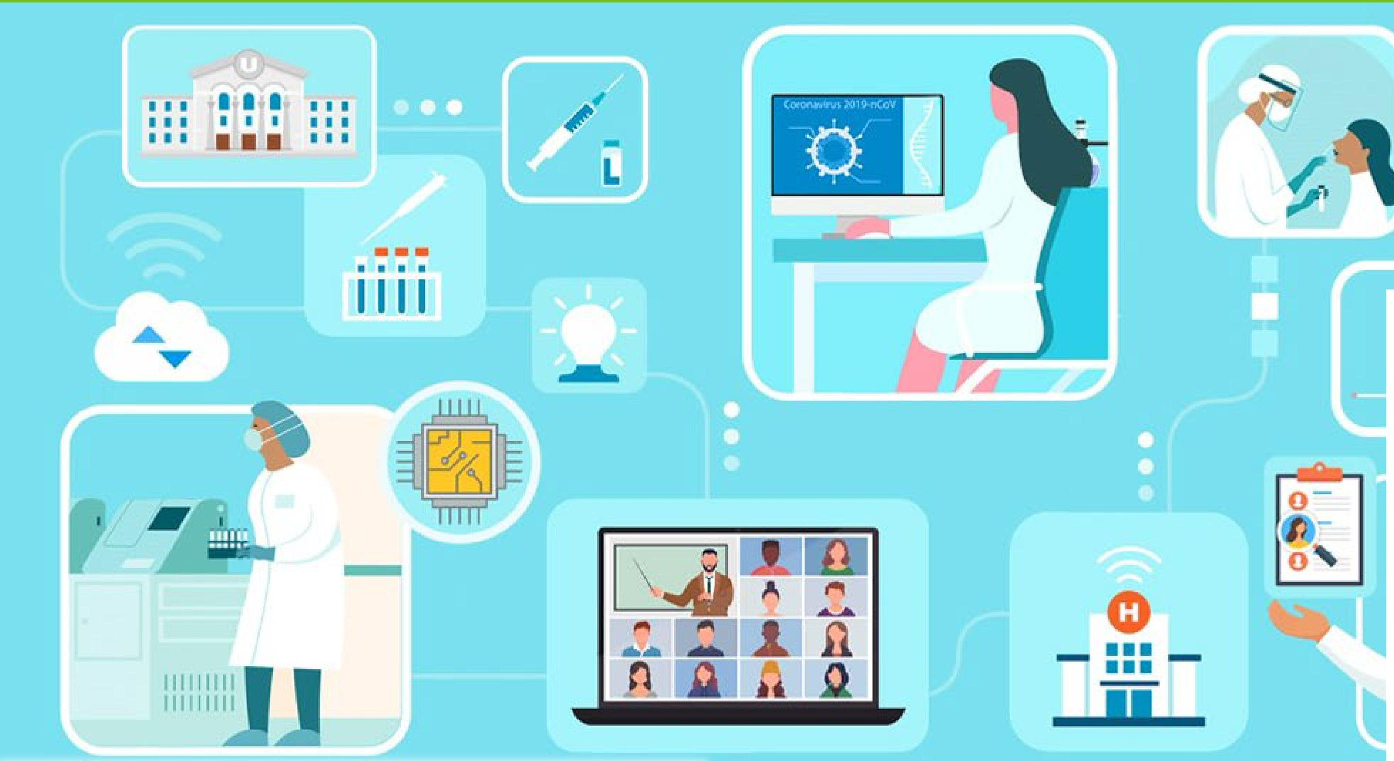
Lehnertz NB, Wang X, Garfin J, Taylor J, Zipprich J, VonBank B, et al. Transmission Dynamics of Severe Acute Respiratory Syndrome Coronavirus 2 in High-Density Settings, Minnesota, USA, March–June 2020. Emerg Infect Dis. 2021;27(8):2052-2063. https://doi.org/10.3201/eid2708.204838

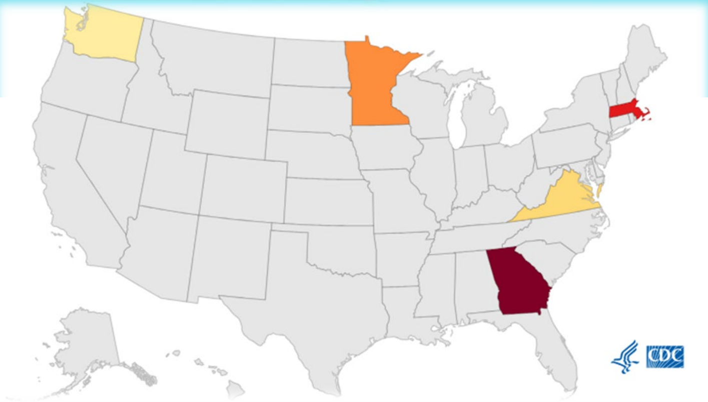
Group A *Streptococcus* Outbreak in Long-Term Care Facility

- GAS outbreak in a long-term care facility H
- WGS of isolates by CDC using CDC developed “cluster tool”, identified cluster of 43 GAS cases in 17 facilities (including facility H) over 3 years
- Epidemiologists re-reviewed cases and interviewed facilities
- Conducted comparison of shared services between facilities with and without cases
- Investigation identified a specific wound provider that serviced multiple facilities



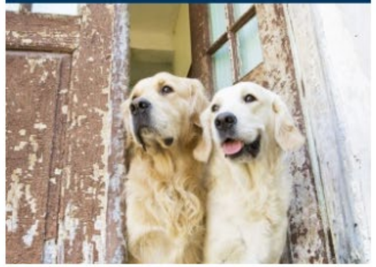
Pathogen Genomics Centers of Excellence





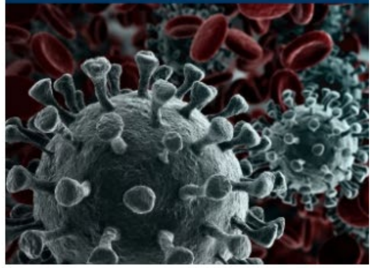
DEPARTMENT
OF HEALTH

People, Pets, and Plasmids

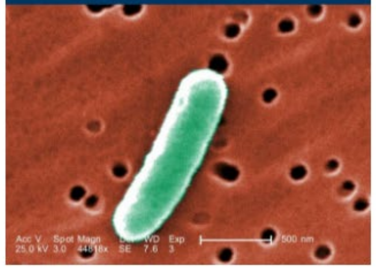


Predicting *Salmonella* Outbreaks

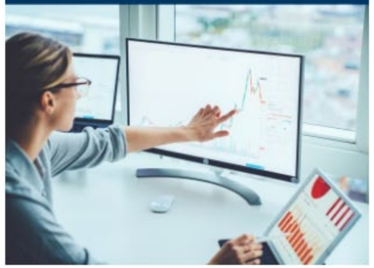
Respiratory Illness in Underserved Communities



Sources of Foodborne Illness Outbreaks



Using COVID-19 Data to Improve Disease Response



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Carlota Medus

Joshua Rounds

Amy Saupe

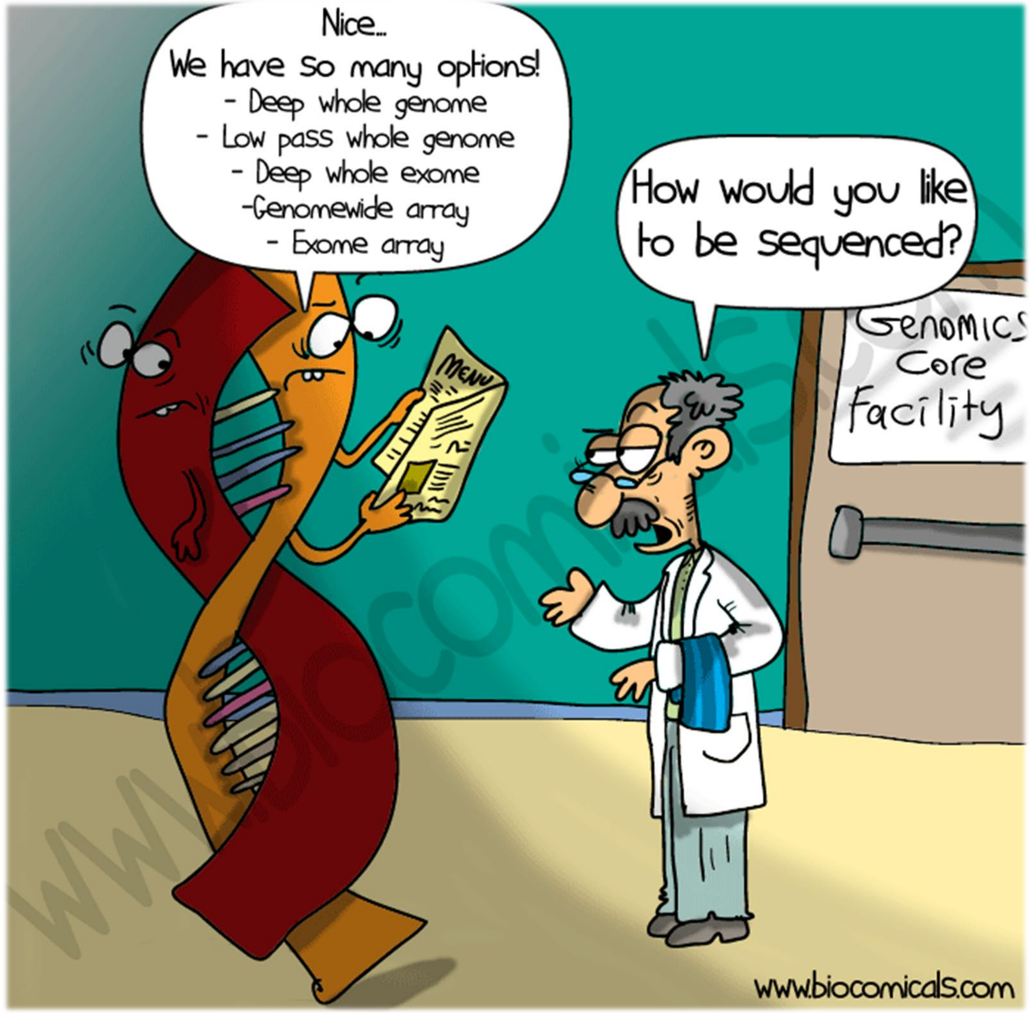
Kirk Smith

Sara Vetter

Sean Wang

and CDC, U MN colleagues and the many others who have worked on pathogen genomics in public health

Thank You!


Nice...
We have so many options!
- Deep whole genome
- Low pass whole genome
- Deep whole exome
-Genomewide array
- Exome array
How would you like to be sequenced?
MENU
Genomics Core Facility
www.biocomicals.com